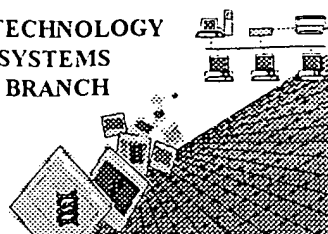BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/026,106A_

Source: _CIPE_

Date Processed by STIC: _7/23/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER
VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *10/026,106 A*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

```
 1 <110> APPLICANT: Renauld, Jean-Christophe
 2          Fickensicher, Helmut
 3          Dumoutier, Laure
 4          Hor, Simon
 6 <120> TITLE OF INVENTION: Isolated Cytokine Receptor LICR-2
 8 <130> FILE REFERENCE: LUD 5752 NDH
10 <140> CURRENT APPLICATION NUMBER: US/10/026,106A
12 <141> CURRENT FILING DATE: 2002-07-01
14 <160> NUMBER OF SEQ ID NOS: 19
```

Does Not Comply
Corrected Diskette Needed

see pp 1-7

ERRORED SEQUENCES

```
      32 <210> SEQ ID NO: 3          19 shown
      33 <211> LENGTH: (20)
      34 <212> TYPE: DNA
      35 <213> ORGANISM: Homo sapiens
W-->  36 <220> FEATURE:
W-->  37 <400> SEQUENCE: 3
E-->  38 aaggccatgg cgggcccga                                    (20) 19
      40 <210> SEQ ID NO: 4
      41 <211> LENGTH: (20) 19
      43 <212> TYPE: DNA
      44 <213> ORGANISM: Homo sapiens
W-->  45 <220> FEATURE:
W-->  46 <400> SEQUENCE: 4
E-->  47 cagaaggtca gtgctgaag
      65 <210> SEQ ID NO: 7      mandatory response needed  (20) 19
E-->  66 <211> LENGTH:
      67 <212> TYPE: DNA
      68 <213> ORGANISM: Homo sapiens
W-->  69 <220> FEATURE:
W-->  70 <400> SEQUENCE: 7
      71 aaggccatgg cggggcccga gcgctggggc cccctgctcc tgtgcctgct gcaggccgct    60
      72 ccagggaggc cccgtctggc ccctccccag aatgtgacgc tgctctccca gaacttcagc   120
      73 gtgtacctga catggctcc cagggcttggc aaccccccag atgtgaccta ttttgtggcc   180
E-->  74 atcagagct ctcccacccg tagacggtgg cgcgaagtgg aagagtgtgc gggaaccaag   (240) 239
E-->  75 gagctgctat gttctatgat gtgcctgaag aaacaggacc tgtacaacaa gttcaaggga   300
E-->  76 cgcgtgcgga cggtttctcc cagctccaag tccccctgg gtggagtcga atacctggat   360
E-->  77 tacctttttg aagtggagcc ggccccacct gtcctggtgc tcaccagac ggaggagat    420
E-->  78 cctgagtgcca atgccacgta ccagctgccc ccctgcatgc ccccactgga tctgaagtat   480
E-->  79 gaggtggcat tctggaagga gggggccgga aacaagaccc tatttccagt cactccccat   540
E-->  80 ggccagccag tccagatcac tctccagcca gctgccagcg aacaccactg cctcagtgcc   600
```

number off

RAW SEQUENCE LISTING   DATE: 07/23/2002
PATENT APPLICATION: US/10/026,106A   TIME: 15:57:08

              Input Set : A:\PTO.VSK.txt
              Output Set: N:\CRF3\07232002\J026106A.raw

```
E--> 81 agaaccatct acacgttcag tgtcccgaaa tacagcaagt tctctaagcc cacctgcttc    660
E--> 82 ttgctggagg tcccagaagc caactgggct ttcctggtgc tgccatcgct tctgatactg    720
E--> 83 ctgttagtaa ttgccgcagg gggtgtgatc tggaagaccc tcatggggaa cccctggttt    780
E--> 85 cagcgggcaa agatgccacg ggccctggac ttttctggac acacacaccc tgtggcaacc    840
E--> 86 tttcagccca gcagaccaga gtccgtgaat gacttgttcc tctgtcccca aaaggaactg    900
E--> 87 accagagggg tcaggccgac gcctcgagtc agggccccag ccacccaaca gacaagatgg    960
E--> 88 aagaaggacc ttgcagagga cgaagaggag gaggatgagg aggacacaga agatggcgtc   1020
E--> 89 agcttccagc cctacattga accaccttct ttcctggggc aagagcacca ggctccaggg   1080
E--> 90 cactcggagg ctggtggggt ggactcaggg aggcccaggg ctcctctggt cccaagcgaa   1140
E--> 91 ggctcctctg cttgggattc ttcagacaga agctgggcca gcactgtgga ctcctcctgg   1200
E--> 92 gacagggctg ggtcctctgg ctatttggct gagaaggggc caggccaagg gccgggtggg   1260
E--> 93 gatgggcacc aagaatctct cccaccacct gaattctcca aggactcggg tttcctggaa   1320
E--> 94 gagctcccag aagataacct ctcctcctgg gccacctggg gcaccttacc accggagccg   1380
E--> 95 aatctggtcc ctgggggacc cccagtttct cttcagacac tgaccttctg ctgggaaagc   1440
E--> 96 agccctgagg aggaagagga ggcgagggaa tcagaaattg aggacagcga tgcgggcagc   1500
E--> 97 tggggggctg agagcacccca gaggaccgag gacaggggcc ggacattggg gcattacatg   1560
E--> 98 gccaggtgag ctgtcccccg acatcccacc gaatctgatg   1600
    101 <210> SEQ ID NO: 8
    102 <211> LENGTH: 522
    103 <212> TYPE: PRT
    104 <213> ORGANISM: Homo sapiens
W--> 105 <220> FEATURE:
W--> 106 <400> SEQUENCE: 8
    107 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
E--> 108
                            5                        10
    109 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
E--> 110
                        20                       25                    30
    111 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
E--> 112               35                       40                    45
    113 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
E--> 114         50                       55                       60
    115 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
E--> 116
    65                      70                       75
    117   Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
E--> 118
                    85                       90
    119 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
E--> 120               100                      105                      110
    121 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
E--> 122               115                      120                      125
    123 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
E--> 124         130                      135                      140
    126 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
E--> 127 145                      150                      155      160
    128 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
E--> 129
                    165                      170                      175
    130 Pro His Val Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro
E--> 131             180                      185                      190
    132 Ala Ala Ser Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe
```

(handwritten annotations: "nos. off", "misaligned amino acid numbering—see item 3 on Errata Summary Sheet")

E--> 133   195   200   205
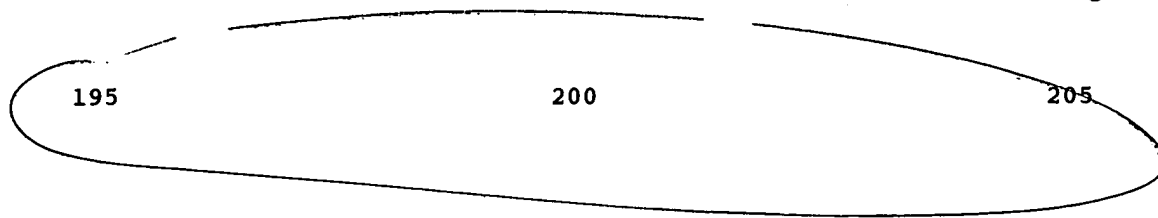
misaligned

     134 Ser Val Pro Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu
E--> 135   210   215   220 **nos.**
     136 Glu Val Pro Glu Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu
E--> 137
225   230   235   2
     138 Ile Leu Leu Leu Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu
E--> 139
                         245   250   255
     140 Met Gly Asn Pro Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp
E--> 141
                         260   265   270
     142 Phe Ser Gly His Thr Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg
E--> 143   275   280   285
     144 Pro Glu Ser Val Asn Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr
E--> 145   290   295   300
     146 Arg Gly Val Arg Pro Thr Pro Arg Val Arg Pro Ala Thr Gln Gln Thr
E--> 147
305   310   315
     148 Arg Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Thr Glu
E--> 149
                         325   330   33
     150 Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly
E--> 151   340   345   350
     152 Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser
E--> 153   355   360   365
     154 Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp
E--> 155   370   375   380
     156 Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp
E--> 157
385   390   395   400
     158 Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly
E--> 159
                         405   410   415
     160 Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser
E--> 161   420   425   430
     162 Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser
E--> 163   435   440   445
     164 Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Pro Asn Leu Val Pro
E--> 165   450   455   460
     168 Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser
E--> 169
465   470   475   4
     170 Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser
E--> 171
                         485   490   495
     172 Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg
E--> 173
                         500   505   510
E--> 174
Gly Arg Thr Leu Gly His Tyr Met Ala Arg .   515   520
     212 <210> SEQ ID NO: 10
     213 <211> LENGTH: 244
     214 <212> TYPE: PRT

```
    215 <213> ORGANISM: Homo sapiens
W--> 216 <220> FEATURE:
W--> 217 <400> SEQUENCE: 10
    219 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
E--> 220
  1                    5                          10                          1
    221 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
E--> 222
                 20                    25                          30
```

misaligned number

RAW SEQUENCE LISTING   DATE: 07/23/2002
PATENT APPLICATION: US/10/026,106A   TIME: 15:57:08

misaligned number

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\07232002\J026106A.raw

```
        223 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
E--> 224            35                        40                              45
        225 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
E--> 226            50                        55                60
        227 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
65                            70                        75
        229 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
E--> 230                      85                        90
        231 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
E--> 232                      100                       105                    110
        233 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
E--> 234            115                       120                 125
        235 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
E--> 236       130                       135                 140
        237 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
E--> 238
145                           150                       155
        239 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
E--> 240
                              165                       170                    175
        241 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
E--> 242                      180                       185                    190
        243 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
E--> 244            195                       200                 205
        245 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Gly
E--> 246       210                       215                 220
        249 Leu Phe Trp Thr His Thr Pro Cys Gly Asn Leu Ser Ala Gln Gln Thr
E--> 250
225                           230                       235                    2
        251 Arg Val Arg Glu
        261 <210> SEQ ID NO: 12
        262 <211> LENGTH: (20)21
        263 <212> TYPE: DNA
        264 <213> ORGANISM: Homo sapiens
W--> 265 <220> FEATURE:
W--> 266 <400> SEQUENCE: 12
E--> 267 aagaaggtgg ttcaatgttag                              (20)21
        295 <210> SEQ ID NO: 16
        296 <211> LENGTH: 24
        297 <212> TYPE: DNA
        298 <213> ORGANISM: Homo sapiens
W--> 299 <220> FEATURE:                    change to
E--> 300 <400> SEQUENCE: (24)16 <-----
        301 gctccatggg acgatgccgc tgtg                        24
```

see next page for more errors

```
<210> 19
<211> 20
<212> DNA
<220>
<400>    19
cactgcattc tagttgtggt                                    20
<213> Homo sapiens
```
move up

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\07232002\J026106A.raw**

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:283 W: Missing Blank Line separator, <220> field identifier
L:21 M:283 W: Missing Blank Line separator, <400> field identifier
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:283 W: Missing Blank Line separator, <220> field identifier
L:37 M:283 W: Missing Blank Line separator, <400> field identifier
L:38 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:19 SEQ:3
L:38 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:19 SEQ:3
L:45 M:283 W: Missing Blank Line separator, <220> field identifier
L:46 M:283 W: Missing Blank Line separator, <400> field identifier
L:47 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:19 SEQ:4
L:47 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:19 SEQ:4
L:53 M:283 W: Missing Blank Line separator, <220> field identifier
L:54 M:283 W: Missing Blank Line separator, <400> field identifier
L:61 M:283 W: Missing Blank Line separator, <220> field identifier
L:62 M:283 W: Missing Blank Line separator, <400> field identifier
L:66 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:69 M:283 W: Missing Blank Line separator, <220> field identifier
L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:74 M:254 E: No. of Bases conflict, LENGTH:Input:240 Counted:239 SEQ:7
M:254 Repeated in SeqNo=7
L:98 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:1599 SEQ:7
L:105 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:174 M:252 E: No. of Seq. differs, <211> LENGTH:Input:522 Found:512 SEQ:8
L:180 M:283 W: Missing Blank Line separator, <220> field identifier
L:181 M:283 W: Missing Blank Line separator, <400> field identifier
L:216 M:283 W: Missing Blank Line separator, <220> field identifier
L:217 M:283 W: Missing Blank Line separator, <400> field identifier
L:220 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:257 M:283 W: Missing Blank Line separator, <220> field identifier
L:258 M:283 W: Missing Blank Line separator, <400> field identifier
L:265 M:283 W: Missing Blank Line separator, <220> field identifier
L:266 M:283 W: Missing Blank Line separator, <400> field identifier
L:267 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:21 SEQ:12
L:267 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:21 SEQ:12
L:273 M:283 W: Missing Blank Line separator, <220> field identifier
L:274 M:283 W: Missing Blank Line separator, <400> field identifier
L:281 M:283 W: Missing Blank Line separator, <220> field identifier
L:282 M:283 W: Missing Blank Line separator, <400> field identifier
L:292 M:283 W: Missing Blank Line separator, <400> field identifier
L:299 M:283 W: Missing Blank Line separator, <220> field identifier
L:300 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:16 differs:24
```

VERIFICATION SUMMARY   DATE: 07/23/2002
PATENT APPLICATION: US/10/026,106A   TIME: 15:57:09

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\07232002\J026106A.raw**

```
L:300 M:283 W: Missing Blank Line separator, <400> field identifier
L:307 M:283 W: Missing Blank Line separator, <220> field identifier
L:308 M:283 W: Missing Blank Line separator, <400> field identifier
L:315 M:283 W: Missing Blank Line separator, <220> field identifier
L:316 M:283 W: Missing Blank Line separator, <400> field identifier
L:322 M:283 W: Missing Blank Line separator, <220> field identifier
L:323 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:323 M:283 W: Missing Blank Line separator, <400> field identifier
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